

Input file Fbh18903FL.seq; Output File 18903.trans  
Sequence length 1983

```

CCTTTAGCCAATTTCGGCCGAGGCCTCCCGCCCCAGTACTTGCTGGCAGGGATTAAGAGCAGATAAAAGTGTGCTCACAC
      M  P  S  T  V  L  P  S  T  V  L  P  S  L  L      15
ACTGTAGACACGGCTACC ATG CCA TCC ACA GTG TTG CCA TCC ACA GTG TTG CCA TCA CTC CTG      45

P  T  A  G  A  G  W  S  M  R  W  I  L  C  W  S  L  T  L  C      35
CCC ACA GCA GGA GCT GGC TGG AGC ATG AGG TGG ATT CTG TGC TGG AGC CTC ACC CTC TGC      105

L  M  A  Q  T  A  L  G  A  L  H  T  K  R  P  Q  V  V  T  K      55
CTG ATG GCG CAG ACG GCC TTG GGT GCC TTG CAC ACC AAG AGG CCT CAA GTG GTC ACC AAA      165

Y  G  T  L  Q  G  K  Q  M  H  V  G  K  T  P  I  Q  V  F  L      75
TAT GGA ACC CTG CAA GGA AAA CAG ATG CAT GTG GGG AAG ACA CCC ATC CAA GTC TTT TTA      225

G  V  P  F  S  R  P  P  L  G  I  L  R  F  A  P  P  E  P  P      95
GGA GTC CCC TTC TCC AGA CCT CCT CTA GGT ATC CTC AGG TTT GCA CCT CCA GAA CCC CCG      285

P  W  K  G  I  R  D  A  T  T  Y  P  P  G  C  L  Q  E  S      115
GAG CCC TGG AAA GGA ATC AGA GAT GCT ACC ACC TAC CCG CCT GGG TGC CTG CAG GAG TCC      345

G  Q  L  A  S  M  Y  V  S  T  R  E  R  Y  K  W  L  R  F      135
TGG GGC CAG CTG GCC TCG ATG TAC GTC AGC ACG CGG GAA CGG TAC AAG TGG CTG CGC TTC      405

S  E  D  C  L  Y  L  N  V  Y  A  P  A  R  A  P  G  D  P  Q      155
AGC GAG GAC TGT CTG TAC CTG AAC GTG TAC GCG CCG GCG CGC GCG CCC GGG GAT CCC CAG      465

P  V  M  V  W  F  P  G  G  A  F  I  V  G  A  A  S  S  Y      175
CTG CCA GTG ATG GTC TGG TTC CCG GGA GGC GCC TTC ATC GTG GGC GCT GCT TCT TCG TAC      525

G  S  D  L  A  A  R  E  K  V  V  L  V  F  L  Q  H  R  L      195
GAG GGC TCT GAC TTG GCC GCC CGC GAG AAA GTG GTG CTG GTG TTT CTG CAG CAC AGG CTC      585

G  I  F  G  F  L  S  T  D  D  S  H  A  R  G  N  W  G  L  L      215
GGC ATC TTC GGC TTC CTG AGC ACG GAC GAC AGC CAC GCG CGC GGG AAC TGG GGG CTG CTG      645

D  Q  M  A  A  L  R  W  V  Q  E  N  I  A  A  F  G  G  D  P      235
GAC CAG ATG GCG GCT CTG CGC TGG GTG CAG GAG AAC ATC GCA GCC TTC GGG GGA GAC CCA      705

G  N  V  T  L  F  G  Q  S  A  G  A  M  S  I  S  G  L  M  M      255
GGA AAT GTG ACC CTG TTC GGC CAG TCG GCG GGG GCC ATG AGC ATC TCA GGA CTG ATG ATG      765

S  P  L  A  S  G  L  F  H  R  A  I  S  Q  S  G  T  A  L  F      275
TCA CCC CTA GCC TCG GGT CTC TTC CAT CGG GCC ATT TCC CAG AGT GGC ACC GCG TTA TTC      825

R  L  F  I  T  S  N  P  L  K  V  A  K  K  V  A  H  L  A  G      295
AGA CTT TTC ATC ACT AGT AAC CCA CTG AAA GTG GCC AAG AAG GTT GCC CAC CTG GCT GGA      885

C  N  H  N  S  T  Q  I  L  V  N  C  L  R  A  L  S  G  T  K      315
TGC AAC CAC AAC AGC ACA CAG ATC CTG GTA AAC TGC CTG AGG GCA CTA TCA GGG ACC AAG      945

V  M  R  V  S  N  K  M  R  F  L  Q  L  N  F  Q  R  D  P  E      335
GTG ATG CGT GTG TCC AAC AAG ATG AGA TTC CTC CAA CTG AAC TTC CAG AGA GAC CCG GAA      1005

E  I  I  W  S  M  S  P  V  V  D  G  V  V  I  P  D  D  P  L      355
GAG ATT ATC TGG TCC ATG AGC CCT GTG GTG GAT GGT GTG GTG ATC CCA GAT GAC CCT TTG      1065

```

Figure 1A

V	L	L	T	Q	G	K	V	S	S	V	P	Y	L	L	G	V	N	N	L	375
GTG	CTC	CTG	ACC	CAG	GGG	AAG	GTT	TCA	TCT	GTG	CCC	TAC	CTT	CTA	GGT	GTC	AAC	AAC	CTG	1125
E	F	N	W	L	L	P	Y	I	M	K	F	P	L	N	R	Q	A	M	R	395
GAA	TTC	AAT	TGG	CTC	TTG	CCT	TAT	ATC	ATG	AAG	TTC	CCG	CTA	AAC	CGG	CAG	GCG	ATG	AGA	1185
K	E	T	I	T	K	M	L	W	S	T	R	T	L	L	N	I	T	K	E	415
AAG	GAA	ACC	ATC	ACT	AAG	ATG	CTC	TGG	AGT	ACC	CGC	ACC	CTG	TTG	AAT	ATC	ACC	AAG	GAG	1245
Q	V	P	L	V	V	E	E	Y	L	D	N	V	N	E	H	D	W	K	M	435
CAG	GTA	CCA	CTT	GTG	GTG	GAG	GAG	TAC	CTG	GAC	AAT	GTC	AAT	GAG	CAT	GAC	TGG	AAG	ATG	1305
L	R	N	R	M	M	D	I	V	Q	D	A	T	F	V	Y	A	T	L	Q	455
CTA	CGA	AAC	CGT	ATG	ATG	GAC	ATA	GTT	CAA	GAT	GCC	ACT	TTC	GTG	TAT	GCC	ACA	CTG	CAG	1365
T	A	H	Y	H	R	D	A	G	L	P	V	Y	L	Y	E	F	E	H	H	475
ACT	GCT	CAC	TAC	CAC	CGA	GAT	GCC	GGC	CTC	CCT	GTC	TAC	CTG	TAT	GAA	TTT	GAG	CAC	CAC	1425
A	R	G	I	I	V	K	P	R	T	D	G	A	D	H	G	D	E	M	Y	495
GCT	CGT	GGA	ATA	ATC	GTC	AAA	CCC	CGC	ACT	GAT	GGG	GCA	GAC	CAT	GGG	GAT	GAG	ATG	TAC	1485
L	F	G	G	P	F	A	T	G	L	S	M	G	K	E	K	A	L	S		515
TTC	CTC	TTT	GGG	GGC	CCC	TTC	GCC	ACA	GGC	CTT	TCC	ATG	GGT	AAG	GAG	AAG	GCA	CTT	AGC	1545
Q	M	M	K	Y	W	A	N	F	A	R	T	G	N	P	N	D	G	N		535
CAG	ATG	ATG	AAA	TAC	TGG	GCC	AAC	TTT	GCC	CGC	ACA	GGA	AAC	CCC	AAT	GAT	GGG	AAT		1605
L	P	C	W	P	R	Y	N	K	D	E	K	Y	L	Q	L	D	F	T	T	555
CTG	CCC	TGC	TGG	CCA	CGC	TAC	AAC	AAG	GAT	GAA	AAG	TAC	CTG	CAG	CTG	GAT	TTT	ACC	ACA	1665
R	V	G	M	K	L	K	E	K	K	M	A	F	W	M	S	L	Y	Q	S	575
AGA	GTG	GGC	ATG	AAG	CTC	AAG	GAG	AAG	AAG	ATG	GCT	TTT	TGG	ATG	AGT	CTG	TAC	CAG	TCT	1725
Q	R	P	E	K	Q	R	Q	F	*											585
CAA	AGA	CCT	GAG	AAG	CAG	AGG	CAA	TTC	TAA											1755

GGGTGGCTATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCATGGACATACC

TGGGGACAAGAGTTCTACCCAAGGGCGAATTCGTTTAAACCTGCAGGACTAG

**Figure 1B**



# Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam5.5/Pfam

Sequence file: /prod/ddm/wspace/orfanal/oa-script.26660.seq

Query: 18903

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
COesterase	Carboxylesterases	558.6	4.1e-164	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
COesterase	1/1	25	569	1	612	558.6	4.1e-164

Alignments of top-scoring domains:

COesterase: domain 1 of 1, from 25 to 569: score 558.6, E = 4.1e-164

```
*->mvlilllflLllllllliavlaaakapedpllVatnnVlcGkvrGvnek
      +l+ +L l l ++ +l+a+++ ++ V t++ G++ G++
18903 25  RWILCWSLTLCLMAQTALGALHT---KRPQVVTKY---GTLQGKQMH 65

      tdngeqsvysFlGIPYAePPVGnLRFkaPqPYkepWsdvldAtkyppsCl
      + ++ +FlG+P+ PP+G LRF +P+P +epW++++dAt+ypp Cl
18903 66  VGKT--PIQVFLGVFPSRPPLGILRFAPPEP-PEPWKGIRDATTYPGCL 112

      QdddfgfsldLKvalkmllslgwnklvg....lklsEDCLYLVNvtPknt
      Q + +g+ 1 +++ ++ + + l +sEDCLYLVNvy P+ +
18903 113 Q-ESWQG-----LASMYVSTRerykwLRFSEDCLYLVNvyAPARA 150

      kpnsklPVmVwIhGGGFmfGsgshlplslydgeslaregnVIvVsiniYRL
      + + +lPVmVw +GG+F +G++ s+Y g+ la++++V++V ++ RL
18903 151 PGDPQLPVMVWFPGGAFIVGAA-----SSYEGSDLAAREKVVLFVLFQHRL 195

      GplGFLstgddklpgsGNyGLlDQrlALkWWqdNiaaFGGDPnsVTifGe
      G++GFLst+d+++ GN+GLlDQ +AL+WWq+NiaaFGGDP++VT+fG+
18903 196 GIFGFLSTDDSHAR--GNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQ 243

      SAGaasVsllllsngGDNppsskgLFhRAIsqSGsalspwaiquesnarg
      SAGa+S+s l++s p++ gLFhRAIsqSG+al +i+s+ +
18903 244 SAGAMSISGLMMS-----PLA-SGLFHRAISQSGTALFRLFITSNP--LK 285

      rakelarllGCnetssselldCLRsksaeeLleatrsfllfeyvpflplf
      ak++a l+GCn++s 1+ CLR s + + + + + f + +f +
18903 286 VAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNN-MRFLQLNFQRDP 334

      l....aFgPvvdGdDapeafipedPeelikeGkfadvPyliGvtdkEGgy
      ++ + +PvvdG+ +ip+dP+ l+ +Gk + vPyl Gv++ E+ +
18903 335 EeiwSMPVVDGV-----VIPDDPLVLLTQGVSSVPYLLGVNNLEFNW 379
```

Figure 3A

```

faamllnasskgedelkktndpvdwlellkyllfyasealnikdMddlad
++++ +++ + + ket ++ l+ ll+ + + +
18903 380 LLPYIMKFPLNR-QAMRKETITK-MLWSTRLLN-ITKEQ-----VP 418

kvlekYpgdvddfsvesrkpnlgdmltDl1FkcptrvaadlhakhggsPv
v e+Y++ v + + ++ + d++ D +F+++ + ++ +++g Pv
18903 419 LVVEEYLDNVNEHDWKMLRNRMMDIVQDATFVYA-TLQTAHYHRDAGLPV 467

YaYvfdhpdasfgigQflakrvdpefggavHgdEiffvFgnpllkeqlyka
Y+Y+f h+a+ + v+p+++ga+HgdE++f+Fg p+ ++ l
18903 468 YLYEFEHHAR-----GIIVKPRTDGADHGDEMYFLFGGPFATG-LS-- 507

teeeeksssktmmnywanFAktGnPnngtsnglvvWpkytseeqkYsll1
e++s +mm+ywanFA+tgNP n++ +l+ Wp y+++e +l+
18903 508 MGKEKALS-LQMMKYWANFARTGNP-NDG--NLPCWPRYNKDEK--YLQL 551

llttitaqklkardprkvlcnfw<-*
+tt +klk+++ ++fw
18903 552 DFTTRVGMKLKEKK-----MAFW 569

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//
Searching for complete domains in SMART

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Figure 3B

GAP of: FrGcgManager\_76\_IOA8lnWg\_ check: 5132 from: 1 to: 1983

Fbh18903FL - Import - vector trimmed

to: FrGcgManager\_76\_JOA3WXZ1\_ check: 1319 from: 1 to: 2456

Z34105 in Patent Nucleotide

Symbol comparison table: /ddm\_local/gcg/gcg\_9.1/gcgcore/data/rundata/nwsgapdna.cmp

CompCheck: 8760

Gap Weight: 12 Average Match: 10.000  
Length Weight: 4 Average Mismatch: 0.000

Quality: 13796 Length: 2746  
Ratio: 6.957 Gaps: 14  
Percent Similarity: 92.617 Percent Identity: 92.617

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 5  
. = 1

FrGcgManager\_76\_IOA8lnWg\_ x FrGcgManager\_76\_JOA3WXZ1\_

COE-2

1 .....CCT 3  
234105 101 CATTTCGCCTTGCTGACGGCGTCGAGCCCTGGCCAGACATGTCCACAGGG 150  
4 TTAGCCAATTCGGCCGAGGCCTCCCGCCCCAGTA.CTTGCTGGCAGGGAT 52  
|| || | ||| | | || || | | || ||  
151 TTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACCGTGGCCGCCGGCGG 200  
53 TAAGAGCAGA.TAAAAGTGTGCTCACACACTGTAGACACGGCTACCATGC 101  
| |||| | || ||| | | ||| ||| || |  
201 GACCAGCACAGGCGGCGTTTCTCCTTCGGAACGGGAACGTCTAGCAACC 250  
102 CATC.....CACAGTGTGCCATCCACAGTGTGCCATCACTCCTGC. 143  
| || | || ||| | | | | |||| ||  
251 CTTCTGTGGGGCTCAATTTTGAAATCTTGAAGTACTTCAACTCCAGCA 300  
144 .CCACAGCAGGAGCT..GGCTGGAGCATGAGGTGGATTCTGTG..CTGGA 188  
| ||| | | || ||| || || ||| || |  
301 ACTACATCTGCTCCTTCAAGTGGTTTGGAAACGGGCTCTTTGGATCTAA 350

Figure 4A



766 GGTGCAGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCC 815  
 ||||||||||||||||||||||||||||||||||||||||  
 1050 GGTGCAGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCC 1099  
  
 816 TGTTCGGCCAGTCGGCGGGGGCCATGAGCATCTCAGGACTGATGATGTCA 865  
 ||||||||||||||||||||||||||||||||||||||||  
 1100 TGTTCGGCCAGTCGGCGGGGGCCATGAGCATCTCAGGACTGATGATGTCA 1149  
  
 866 CCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCCAGAGTGGCACCCGC 915  
 ||||||||||||||||||||||||||||||||||||||||  
 1150 CCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCCAGAGTGGCACCCGC 1199  
  
 916 GTTATTTCAGACTTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGG 965  
 ||||||||||||||||||||||||||||||||||||||||  
 1200 GTTATTTCAGACTTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGG 1249  
  
 966 TTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC 1015  
 ||||||||||||||||||||||||||||||||||||||||  
 1250 TTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC 1299  
  
 1016 TGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGAT 1065  
 ||||||||||||||||||||||||||||||||||||||||  
 1300 TGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGAT 1349  
  
 1066 GAGATTCTCTCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGT 1115  
 ||||||||||||||||||||||||||||||||||||||||  
 1350 GAGATTCTCTCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGT 1399  
  
 1116 CCATGAGCCCTGTGGTGGATGGTGTGGTGATCCCAGATGACCCTTTGGTG 1165  
 ||||||||||||||||||||||||||||||||||||||||  
 1400 CCATGAGCCCTGTGGTGGATGGTGTGGTGATCCCAGATGACCCTTTGGTG 1449  
  
 1166 CTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTTCTAGGTGTCAA 1215  
 ||||||||||||||||||||||||||||||||||||||||  
 1450 CTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTTCTAGGTGTCAA 1499  
  
 1216 CAACCTGGAATTCAATTGGCTCTTGCCTTATATCATGAAGTTCCCGCTAA 1265  
 ||||||||||||||||||||||||||||||||||||  
 1500 CAACCTGGAATTCAATTGGCTCTTGCCTTAT..... 1530  
  
  
 1316 CGCACCCCTGTTGAATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGA 1365  
 ||||||||||||||||||||||||||||||||||||||||  
 1531 .....AATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGA 1568  
  
 1366 GTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTA 1415  
 ||||||||||||||||||||||||||||||||||||||||  
 1569 GTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTA 1618

Figure 4C



1416 TGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCCACTGCAGACT 1465  
 ||||||||||||||||||||||||||||||||||||||||||||  
 1619 TGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCCACTGCAGACT 1668  
 1466 GCTCACTACCACCGAGATGCCGGCCTCCCTGTCTACCTGTATGAATTTGA 1515  
 ||||||||||||  
 1669 GCTCACTACCACCGA..... 1683  
  
 1666 CAACTTTGCCCCGACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGGC 1715  
 ||||||||||||||||||||||||||||||||||||||||  
 1684 .....GAAACCCCAATGATGGGAATCTGCCCTGCTGGC 1716  
 1716 CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGA 1765  
 ||||||||||||||||||||||||||||||||||||||||  
 1717 CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGA 1766  
 1766 GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTGGATGAGTCTGTA 1815  
 ||||||||||||||||||||||||||||||||||||||||  
 1767 GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTGGATGAGTCTGTA 1816  
 1816 CCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCA 1865  
 ||||||||||||||||||||||||||||||||||||||||  
 1817 CCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCA 1866  
 1866 GGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGAC 1915  
 ||||||||||||||||||||||||||||||||||||||||  
 1867 GGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGAC 1916  
 1916 TAGCCATGGACATACCTGGGGACAAGAGTTCTACCCAAGGGCGAATTCGT 1965  
 |||||||||||||||||||||||||||||||| | |  
 1917 TAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA...CCCCA...GT 1960  
 1966 TTAAACCTGCAGGA.CTAG..... 1983  
 || | ||||||||  
 1961 TTAGAACTGCAGGAGCTCCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTTT 2010

**Figure 4D**

ALIGN calculates a global alignment of two sequences

version 2.0u Please cite: Myers and Miller, CABIOS (1989)

COE-2 584 aa vs.

PRO873 545 aa

scoring matrix: BLOSUM50, gap penalties: -12/-2

62.4% identity; Global alignment score: 2271

```

                                10
COE-2  M-----PST-----VLPSTVLPSSLPTAG
      :               : : : :
PRO873 MSTGFSFGSGTLGSTTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTAPS
      10      20      30      40      50      60

      20      30      40      50      60      70
COE-2  AGWSMRWILCWSLTCLMAQTALGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVPF
      : : : : :
PRO873 SGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVPF
      70      80      90      100     110     120

      80      90      100     110
COE-2  SRPPLGILRFAPPEPPEPWKGIRDATTYPPG-----
      : : : : :
PRO873 SRPPLGILRFAPPEPPEPWKGIRDATTYPPGWSLALSPGWSAVARSRLTATSASRVQASL
      130     140     150     160     170     180

      120     130     140     150
COE-2  -----CLQESWGQLASMYVSTREYKWLRFSEDCLYLN VYAPARAPGDPQLPVM
      : : : : :
PRO873 LPQPLSVWGYRCLQESWGQLASMYVSTREYKWLRFSEDCLYLN VYAPARAPGDPQLPVM
      190     200     210     220     230     240

      160     170     180     190     200     210
COE-2  VWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMA
      : : : : :
PRO873 VWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMA
      250     260     270     280     290     300

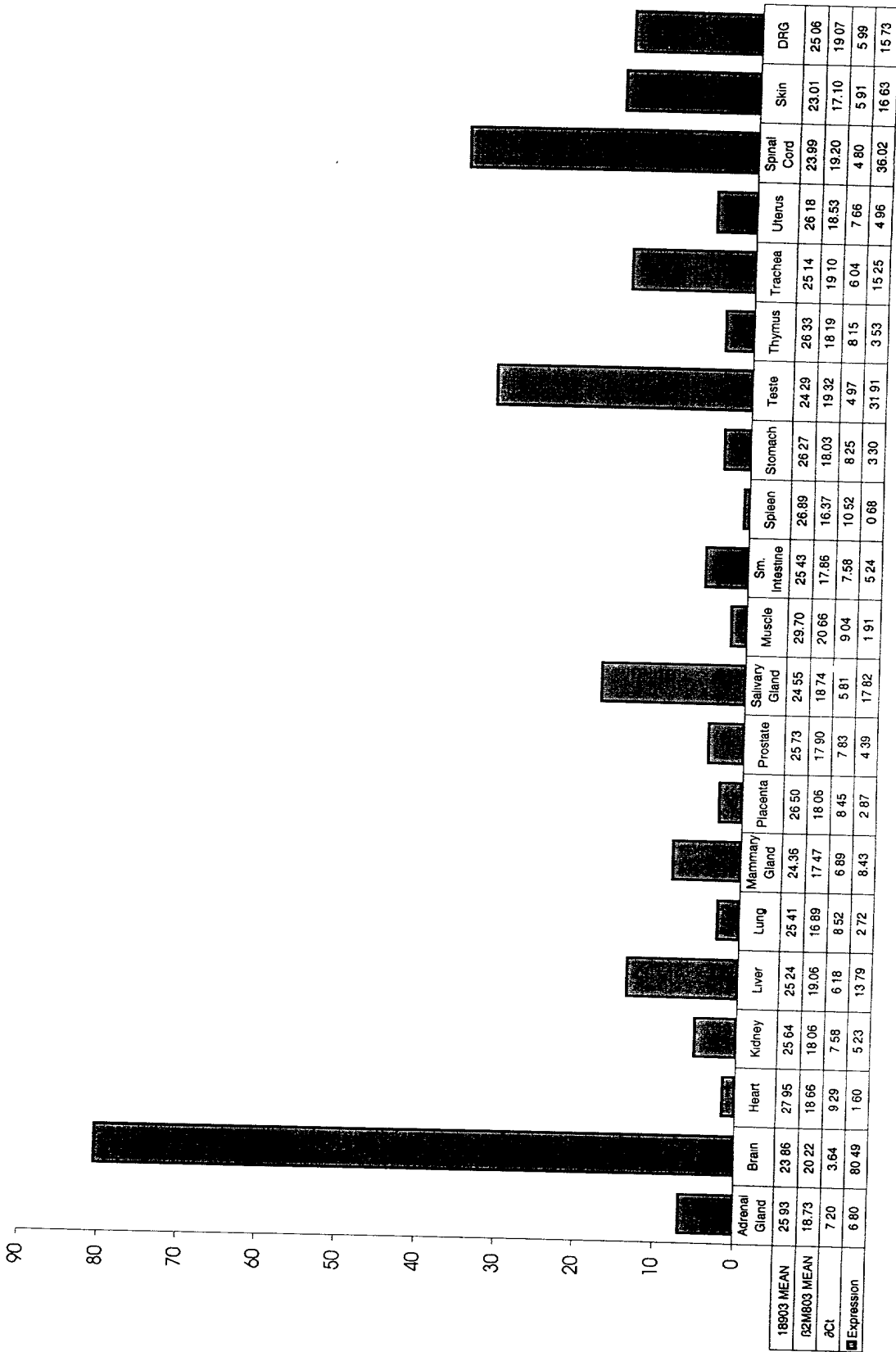
      220     230     240     250     260     270
COE-2  ALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFI
      : : : : :
PRO873 ALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFI
      310     320     330     340     350     360

      280     290     300     310     320     330
COE-2  TSNPLKVAKKVAHLAGCNHNSTQILVNCLRALS GTKVMRVS NKMRFLQLNFQRDPEEIIW
      : : : : :
PRO873 TSNPLKVAKKVAHLAGCNHNSTQILVNCLRALS GTKVMRVS NKMRFLQLNFQRDPEEIIW
      370     380     390     400     410     420
```

Figure 5A

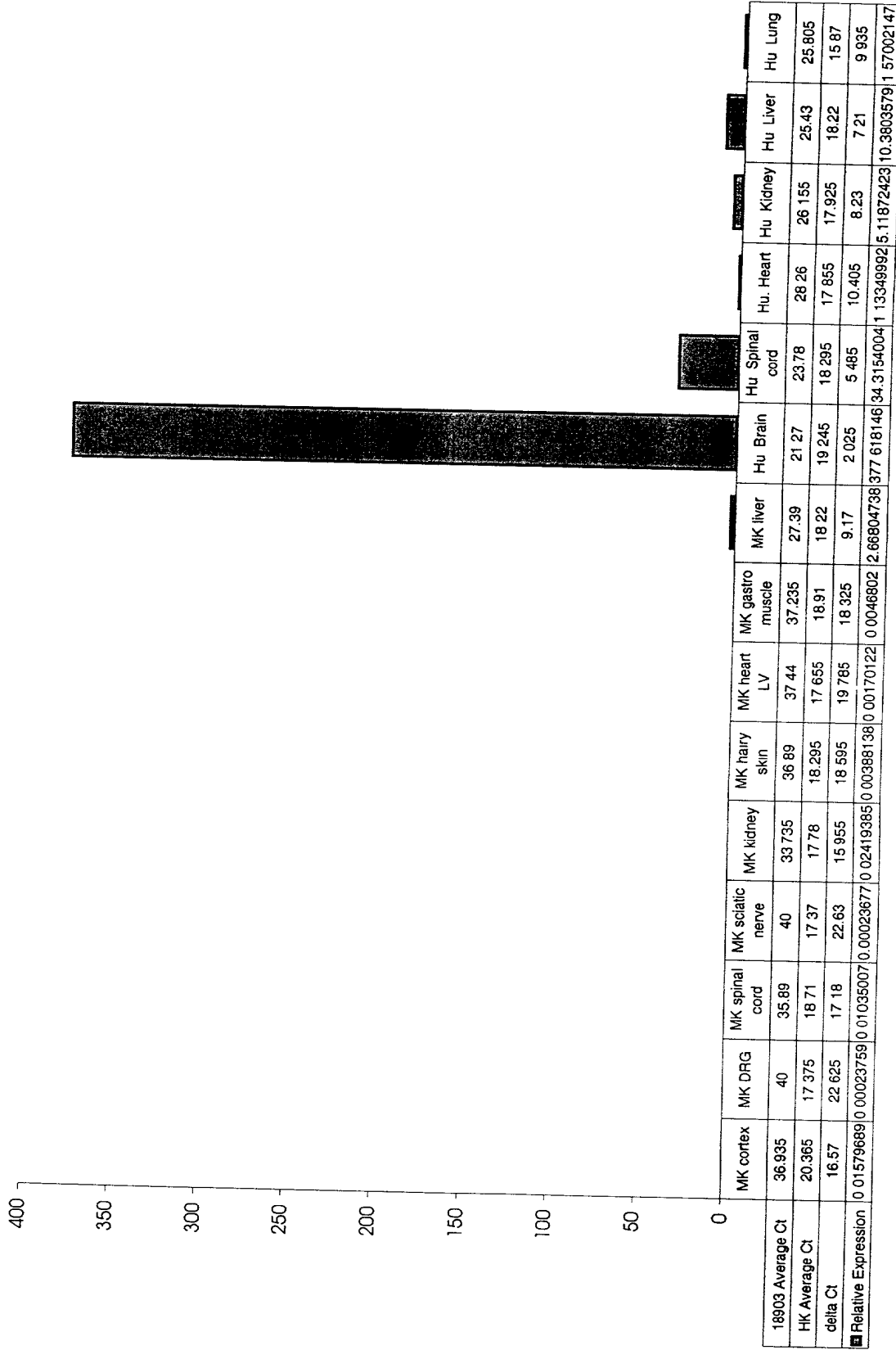


Figure 6



18903 Average Ct 36.935  
 HK Average Ct 20.365  
 delta Ct 16.57  
 Relative Expression 0.01579689

Figure 7





**Figure 8B**

Tissue	18903 MEAN	B2M803 MEAN • Ct	Expression	
Fetal heart/ normal	31.89	19.68	12.21	0.21
Aorta / normal	36.11	22.53	13.58	0.00
Heart normal	31.54	17.89	13.65	0.08
Heart/ CHF	31.50	19.45	12.05	0.24
Vein/ Normal	36.01	18.99	17.02	0.00
SMC (Aortic)	31.76	18.74	13.02	0.12
Spinal cord/ Normal	33.06	21.40	11.66	0.31
Brain cortex/ Normal	29.68	20.58	9.10	1.83
Brain hypothalamus/ Normal	29.45	19.24	10.21	0.85
Glial cells (Astrocytes)	33.94	21.09	12.86	0.13
Brain/ Glioblastoma	30.39	17.43	12.97	0.13
Breast/ Normal	30.10	18.60	11.50	0.35
Breast tumor/ IDC	30.75	17.66	13.09	0.11
OVARY/ Normal	31.73	19.95	11.79	0.28
OVARY/ Tumor	33.59	18.91	14.68	0.04
Pancreas	30.88	17.33	13.55	0.08
Prostate/ Normal	31.16	18.34	12.83	0.14
Prostate/ Tumor	29.03	17.57	11.46	0.35
Colon/ normal	32.03	17.78	14.26	0.05
Colon/ tumor	30.80	18.15	12.66	0.16
Colon/ IBD	32.37	17.72	14.65	0.04
Kidney/ normal	30.98	20.03	10.95	0.51
Liver/ normal	31.82	19.08	12.75	0.15
Liver fibrosis	30.10	18.82	11.29	0.40
Fetal Liver/normal	33.55	21.39	12.16	0.22
Lung / normal	30.54	17.31	13.23	0.10
Lung/ tumor	30.30	17.77	12.53	0.17
Lung/ COPD	29.44	17.10	12.34	0.19
Tonsil/ normal	31.13	17.19	13.94	0.06
Lymph node/ normal	31.40	17.91	13.49	0.09
Thymus/ normal	32.80	20.03	12.78	0.14
Epithelial Cells (prostate)	30.70	20.13	10.57	0.66
Endothelial Cells (aortic)	35.27	20.16	15.11	0.03
Skeletal Muscle/ Normal	31.06	18.26	12.81	0.14
Fibroblasts (Dermal)	33.10	18.18	14.92	0.03
Skin/ normal	31.16	20.29	10.87	0.54
Adipose/ Normal	32.43	17.96	14.47	0.04
Osteoblasts (primary)	34.84	20.44	14.40	0.05
Osteoblasts (Undiff)	33.19	18.50	14.69	0.04
Osteoblasts(Diff)	33.23	17.83	15.40	0.02
Osteoclasts	32.47	17.25	15.22	0.03
Aorta SMC (Early)	32.50	19.53	12.97	0.13
Aorta SMC (Late )	32.72	18.77	13.96	0.06
HUVEC	32.17	19.27	12.91	0.13
HMVEC	32.74	18.74	14.00	0.06

40.00 40.00 0.00